



PCT10

**Does Not Comply
Corrected Diskette Needed**

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/019,065

DATE: 07/16/2002

TIME: 13:52:22

Input Set : A:\EP.txt

Output Set: N:\CRF3\07162002\J019065.raw

PatentIn 2.0 "bug". See
p. 7 for explanation

W--> 3 <140> CURRENT APPLICATION NUMBER: US/10/019,065
W--> 0 <160> NUMBER OF SEQ ID NOS:
3 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

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803 <212> TYPE: PRT
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806 <400> SEQUENCE: 33

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| 807 | Thr | Pro | Ile | Gly | Arg | Pro | Arg | Ile | Arg | His | Gln | Asp | Lys | Arg | Thr | Val |
| 808 | 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| 810 | Asp | Leu | Thr | Val | Gln | Val | Pro | Pro | Ser | Ile | Ala | Asp | Glu | Pro | Thr | Asp |
| 811 | | | | 20 | | | | | 25 | | | | 30 | | | |
| 813 | Phe | Leu | Val | Thr | Lys | His | Ala | Pro | Ala | Val | Ile | Thr | Cys | Thr | Ala | Ser |
| 814 | | | 35 | | | | | 40 | | | | | 45 | | | |
| 816 | Gly | Val | Pro | Phe | Pro | Ser | Ile | His | Trp | Thr | Lys | Asn | Gly | Ile | Arg | Leu |
| 817 | | 50 | | | | | 55 | | | | | 60 | | | | |
| 819 | Leu | Pro | Arg | Gly | Asp | Gly | Tyr | Arg | Ile | Leu | Ser | Ser | Gly | Ala | Ile | Glu |
| 820 | 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| 822 | Ile | Leu | Ala | Thr | Gln | Leu | Asn | His | Ala | Gly | Arg | Tyr | Thr | Cys | Val | Ala |
| 823 | | | | | 85 | | | | | 90 | | | | | 95 | |
| 825 | Arg | Asn | Ala | Ala | Gly | Ser | Ala | His | Arg | His | Val | Thr | Leu | His | Val | His |
| 826 | | | | 100 | | | | | 105 | | | | | 110 | | |
| 828 | Glu | Pro | Pro | Val | Ile | Gln | Pro | Gln | Pro | Ser | Glu | Leu | His | Val | Ile | Leu |
| 829 | | | | 115 | | | | 120 | | | | | 125 | | | |
| 831 | Asn | Asn | Pro | Ile | Leu | Leu | Pro | Cys | Glu | Ala | Thr | Gly | Thr | Pro | Ser | Pro |
| 832 | | 130 | | | | | 135 | | | | | 140 | | | | |
| 834 | Phe | Ile | Thr | Trp | Gln | Lys | Glu | Gly | Ile | Asn | Val | Asn | Thr | Ser | Gly | Arg |
| 835 | 145 | | | | 150 | | | | | 155 | | | | | 160 | |
| 837 | Asn | His | Ala | Val | Leu | Pro | Ser | Gly | Gly | Leu | Gln | Ile | Ser | Arg | Ala | Val |
| 838 | | | | 165 | | | | | 170 | | | | | 175 | | |
| 840 | Arg | Glu | Asp | Ala | Gly | Thr | Tyr | Met | Cys | Val | Ala | Gln | Asn | Pro | Ala | Gly |
| 841 | | | | 180 | | | | | 185 | | | | | 190 | | |
| 843 | Thr | Ala | Leu | Gly | Lys | Ile | Lys | Leu | Asn | Val | Gln | Val | Pro | Pro | Val | Ile |
| 844 | | | 195 | | | | | 200 | | | | | 205 | | | |
| 846 | Ser | Pro | His | Leu | Lys | Glu | Tyr | Val | Ile | Ala | Val | Asp | Lys | Pro | Ile | Thr |
| 847 | | 210 | | | | | 215 | | | | | 220 | | | | |
| 849 | Leu | Ser | Cys | Glu | Ala | Asp | Gly | Leu | Pro | Pro | Pro | Asp | Ile | Thr | Trp | His |
| 850 | 225 | | | | 230 | | | | | 235 | | | | | 240 | |
| 852 | Lys | Asp | Gly | Arg | Ala | Ile | Val | Glu | Ser | Ile | Arg | Gln | Arg | Val | Leu | Ser |

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|-----|-------------|-------------------------|-----------------|---------------------|-----|-----|-----|
| 853 | | 245 | | 250 | | 255 | |
| 856 | Ser Gly Ser | Leu Gln Ile Ala Phe Val | Gln Pro Gly Asp | Ala Gly His | | | |
| 857 | | 260 | | 265 | | 270 | |
| 859 | Tyr Thr Cys | Met Ala Ala Asn Val | Ala Gly Ser Ser | Ser Thr Ser Thr | | | |
| 860 | | 275 | | 280 | | 285 | |
| 862 | Lys Leu Thr | Val His Val Pro Pro | Arg Ile Arg Ser | Thr Lys Gly His | | | |
| 863 | | 290 | | 295 | | 300 | |
| 865 | Tyr Thr Val | Asn Glu Asn Ser | Gln Ala Ile Leu | Pro Cys Val Ala Asp | | | |
| 866 | 305 | | 310 | | 315 | | 320 |
| 868 | Gly Ile Pro | Thr Pro Ala Ile Asn | Trp Lys Lys Asp | Asn Val Leu Leu | | | |
| 869 | | 325 | | 330 | | 335 | |
| 871 | Ala Asn Leu | Leu Gly Lys Tyr Thr | Ala Glu Pro Tyr | Gly Glu Leu Ile | | | |
| 872 | | 340 | | 345 | | 350 | |
| 874 | Leu Glu Asn | Val Val Leu Glu Asp | Ser Gly Phe Tyr | Thr Cys Val Ala | | | |
| 875 | | 355 | | 360 | | 365 | |
| 877 | Asn Asn Ala | Ala Gly Glu Asp | Thr His Thr Val | Ser Leu Thr Val His | | | |
| 878 | | 370 | | 375 | | 380 | |
| 880 | Val Leu Pro | Thr Phe Thr Glu Leu | Pro Gly Asp Val | Ser Leu Asn Lys | | | |
| 881 | 385 | | 390 | | 395 | | 400 |
| 883 | Gly Glu Gln | Leu Arg Leu Ser | Cys Lys Ala Thr | Gly Ile Pro Leu Pro | | | |
| 884 | | 405 | | 410 | | 415 | |
| 886 | Lys Leu Thr | Trp Thr Phe Asn Asn | Asn Ile Ile Pro | Ala His Phe Asp | | | |
| 887 | | 420 | | 425 | | 430 | |
| 889 | Ser Val Asn | Gly His Ser Glu Leu | Val Ile Glu Arg | Val Ser Lys Glu | | | |
| 890 | | 435 | | 440 | | 445 | |
| 892 | Asp Ser Gly | Thr Tyr Val Cys | Thr Ala Glu Asn | Ser Val Gly Phe Val | | | |
| 893 | | 450 | | 455 | | 460 | |
| 895 | Lys Ala Ile | Gly Phe Val Tyr Val | Lys Glu Pro Pro | Val Phe Lys Gly | | | |
| 896 | 465 | | 470 | | 475 | | 480 |
| 898 | Asp Tyr Pro | Ser Asn Trp Ile Glu | Pro Leu Gly Gly | Asn Ala Ile Leu | | | |
| 899 | | 485 | | 490 | | 495 | |
| 901 | Asn Cys Glu | Val Lys Gly Asp | Pro Thr Pro Thr | Ile Gln Trp Asn Arg | | | |
| 902 | | 500 | | 505 | | 510 | |
| 904 | Lys Gly Val | Asp Ile Glu Ile Ser | His Arg Ile Arg | Gln Leu Gly Asn | | | |
| 905 | | 515 | | 520 | | 525 | |
| 907 | Gly Ser Leu | Ala Ile Tyr Gly | Thr Val Asn Glu | Asp Ala Gly Asp Tyr | | | |
| 908 | | 530 | | 535 | | 540 | |
| 910 | Thr Cys Val | Ala Thr Asn Glu | Ala Gly Val Val | Glu Arg Ser Met Ser | | | |
| 911 | 545 | | 550 | | 555 | | 560 |
| 913 | Leu Thr Leu | Arg Ser Pro Pro | Ile Ile Thr Leu | Glu Pro Val Glu Thr | | | |
| 914 | | 565 | | 570 | | 575 | |
| 916 | Val Ile Asn | Ala Gly Gly Lys | Ile Ile Leu Asn | Cys Gln Ala Thr Gly | | | |
| 917 | | 580 | | 585 | | 590 | |
| 919 | Glu Pro Gln | Pro Thr Ile Thr | Trp Ser Arg Gln | Gly His Ser Ile Ser | | | |
| 920 | | 595 | | 600 | | 605 | |
| 922 | Trp Asp Asp | Arg Val Asn Val | Leu Ser Asn Asn | Ser Leu Tyr Ile Ala | | | |
| 923 | | 610 | | 615 | | 620 | |
| 925 | Asp Ala Gln | Lys Glu Asp Thr | Ser Glu Phe Glu | Cys Val Ala Arg Asn | | | |
| 926 | 625 | | 630 | | 635 | | 640 |

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928 Leu Met Gly Ser Val Leu Val Arg Val Pro Val Ile Val Gln Val His
929           645           650           655
931 Gly Gly Phe Ser Gln Trp Ser Ala Trp Arg Ala Cys Ser Val Thr Cys
932           660           665           670
934 Gly Lys Gly Ile Gln Lys Arg Ser Arg Leu Cys Asn Gln Pro Leu Pro
935           675           680           685
937 Ala Asn Gly Gly Lys Pro Cys Gln Gly Ser Asp Leu Glu Met Arg Asn
938           690           695           700
940 Cys Gln Asn Lys Pro Cys Pro Val Asp Gly Ser Trp Ser Glu Trp Ser
941 705           710           715           720
943 Leu Trp Glu Glu Cys Thr Arg Ser Cys Gly Arg Gly Asn Gln Thr Arg
944           725           730           735
946 Thr Arg Thr Cys Asn Asn Pro Ser Val Gln His Gly Gly Arg Pro Cys
947           740           745           750
949 Glu Gly Asn Ala Val Glu Ile Ile Met Cys Asn Ile Arg Pro Cys Pro
950           755           760           765
952 Val His Gly Ala Trp Ser Ala Trp Gln Pro Trp Gly Thr Cys Ser Glu
953           770           775           780
955 Ser Cys Gly Lys Gly Thr Gln Thr Arg Ala Arg Leu Cys Asn Asn Pro
956 785           790           795           800
958 Pro Pro Ala Phe Gly Gly Ser Tyr Cys Asp Gly Ala Glu Thr Gln Met
959           805           810           815
961 Gln Val Cys Asn Glu Arg Asn Cys Pro Ile His Gly Lys Trp Ala Thr
962           820           825           830
964 Trp Ala Ser Trp Ser Ala Cys Ser Val Ser Cys Gly Gly Ala Arg
965           835           840           845
967 Gln Arg Thr Arg Gly Cys Ser Asp Pro Val Pro Gln Tyr Gly Gly Arg
968           850           855           860
970 Lys Cys Glu Gly Ser Asp Val Gln Ser Asp Phe Cys Asn Ser Asp Pro
971 865           870           875           880
973 Cys Pro Thr His Gly Asn Trp Ser Pro Trp Ser Gly Trp Gly Thr Cys
974           885           890           895
976 Ser Arg Thr Cys Asn Gly Gly Gln Met Arg Arg Tyr Arg Thr Cys Asp
977           900           905           910
979 Asn Pro Pro Pro Ser Asn Gly Gly Arg Ala Cys Gly Gly Pro Asp Ser
980           915           920           925
982 Gln Ile Gln Arg Cys Asn Thr Asp Met Cys Pro Val Asp Gly Ser Trp
983           930           935           940
985 Gly Ser Trp His Ser Trp Ser Gln Cys Ser Ala Ser Cys Gly Gly Gly
986 945           950           955           960
988 Glu Lys Thr Arg Lys Arg Leu Cys Asp His Pro Val Pro Val Lys Gly
989           965           970           975
991 Gly Arg Pro Cys Pro Gly Asp Thr Thr Gln Val Thr Arg Cys Asn Val
992           980           985           990
994 Gln Ala Cys Pro Gly Gly Pro Gln Arg Ala Arg Gly Ser Val Ile Gly
995           995           1000           1005
997 Asn Ile Asn Asp Val Glu Phe Gly Ile Ala Phe Leu Asn Ala Thr Ile
998 1010           1015           1020
1000 Thr Asp Ser Pro Asn Ser Asp Thr Arg Ile Ile Arg Ala Lys Ile Thr

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1001 1025          1030          1035          1040
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1004          1045          1050          1055
1006 Leu Asn Pro Ile Tyr Trp Thr Thr Ala Lys Glu Ile Gly Glu Ala Val
1007          1060          1065          1070
1009 Asn Gly Phe Thr Leu Thr Asn Ala Val Phe Lys Arg Glu Thr Gln Val
1010          1075          1080          1085
1012 Glu Phe Ala Thr Gly Glu Ile Leu Gln Met Ser His Ile Ala Arg Gly
1013          1090          1095          1100
1015 Leu Asp Ser Asp Gly Ser Leu Leu Leu Asp Ile Val Val Ser Gly Tyr
1016 1105          1110          1115          1120
1018 Val Leu Gln Leu Gln Ser Pro Ala Glu Val Thr Val Lys Asp Tyr Thr
1019          1125          1130          1135
1021 Glu Asp Tyr Ile Gln Thr Gly Pro Gly Gln Leu Tyr Ala Tyr Ser Thr
1022          1140          1145          1150
1024 Arg Leu Phe Thr Ile Asp Gly Ile Ser Ile Pro Tyr Thr Trp Asn His
1025          1155          1160          1165
1027 Thr Val Phe Tyr Asp Gln Ala Gln Gly Arg Met Pro Phe Leu Val Glu
1028          1170          1175          1180
1030 Thr Leu His Ala Ser Ser Val Glu Ser Asp Tyr Asn Gln Ile Glu Glu
1031 1185          1190          1195          1200
1033 Thr Leu Gly Phe Lys Ile His Ala Ser Ile Ser Lys Gly Asp Arg Ser
1034          1205          1210          1215
1036 Asn Gln Cys Pro Ser Gly Phe Thr Leu Asp Ser Val Gly Pro Phe Cys
1037          1220          1225          1230
1039 Ala Asp Glu Asp Glu Cys Ala Ala Gly Asn Pro Cys Ser His Ser Cys
1040          1235          1240          1245
1042 His Asn Ala Met Gly Thr Tyr Tyr Cys Ser Cys Pro Lys Gly Leu Thr
1043          1250          1255          1260
1045 Ile Ala Ala Asp Gly Arg Thr Cys Gln Asp Ile Asp Glu Cys Ala Leu
1046 1265          1270          1275          1280
1048 Gly Arg His Thr Cys His Ala Gly Gln Asp Cys Asp Asn Thr Ile Gly
1049          1285          1290          1295
1051 Ser Tyr Arg Cys Val Val Arg Cys Gly Ser Gly Phe Arg Arg Thr Ser
1052          1300          1305          1310
1054 Asp Gly Leu Ser Cys Gln Asp Ile Asn Glu Cys Gln Glu Ser Ser Pro
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E--> 1058 1330 1335

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1066 <400> SEQUENCE: 34

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1069 gcagtaatta cctgcactgc ttcgggagtt ccatttcctt caattcactg gaccaaaaaat 180
1070 ggtataagac tgcttcccag gggagatggc tatagaattc tgcctcagg agcaattgaa 240
1071 atacttgcca cccaattaaa ccatgctgga agatacactt gtgtcgctag gaatgcggct 300

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1072 ggctctgcac atcgacacgt gacccttcat gttcatgagc ctccagtcac tcagccccc 360
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1074 acaccagtc ctttcattac ttggcaaaaa gaaggcatca atgttaacac ttcaggcaga 480
1075 aaccatgcag ttcttcctag tggcggtta cagatctcca gagctgtccg agaggatgct 540
1076 ggcacttaca tgtgtgtggc ccagaaccgc gctggtacag ccttgggcaa aatcaagtta 600
1077 aatgtccaag ttctccagc cattagccct catctaaagg aatatgttat tgctgtggac 660
1078 aagcccatca cgttatcctg tgaagcagat ggcctccctc cgcctgacat tacatggcat 720
1079 aaagatgggc gtgcaattgt ggaatctatc cgccagcgcg tcctcagctc tggctctctg 780
1080 caaatagcat ttgtccagcc tggatgatgt ggccattaca cgtgcatggc agccaatgta 840
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1082 acaaaaggac actacacggt caatgagaat tcacaagcca ttcttccatg cgtagctgat 960
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1117 cgagccagag gaagtgttat tggaaatatt aatgatgttg aatttggaat tgcttctct 3060
1118 aatgccacaa taactgatag ccctaactct gatactagaa taatacgtgc caaaattacc 3120
1119 aatgtacctc gtagtcttgg ttccagcaatg agaaagatag tttctattct aaatcccat 3180
1120 tattggacaa cagcaaagga aataggagaa gcagtcaatg gctttaccct caccaatgca 3240

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1122 attgcccggg gcttggattc cgatggttct ttgctgctag atatcgttgt gagtggctat 3360
1123 gtcctacagc ttcagtcacc tgctgaagtc actgtaaagg attacacaga ggactacatt 3420
1124 caaacaggtc ctgggcagct gtacgcctac tcaaccggc tggtcaccat tgatggcatc 3480
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1127 acaactgggtt ttaaaattca tgcttcaata tccaaaggag atcgagtaa tcagtgcctc 3660
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1129 gggaatccct gctcccatag ctgccacaat gccatgggga cttactactg ctctgccct 3780
1130 aaaggcctca ccatagtctc agatggaaga acttgtcaag atattgatga gtgtgctttg 3840
1131 ggtaggcata cctgccacgc tggtcaggac tgtgacaata cgattggatc ttatcgctgt 3900
1132 gtggtccgtt gtggaagtgg ctttcgaaga acctctgatg ggctgagttg tcaagatatt 3960
1133 aatgaatgtc aagaatccag ccctgtcacc agcgtgttt caatgccata ggaagtttcc 4020
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E--> 1138 1
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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/019,065

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Input Set : A:\EP.txt

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Seq#:34; Line(s) 1128,1129,1130,1131,1132,1133,1134,1135,1136

PatentIn 2.0 "bug":

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses(as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk. }

VERIFICATION SUMMARY

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Input Set : A:\EP.txt

Output Set: N:\CRF3\07162002\J019065.raw

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L:1138 M:254 E: No. of Bases conflict, this line has no nucleotides.
M:254 Repeated in SeqNo=34
L:0 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (0) Counted (34)